

SEQUENCE LISTING

SEQ ID NO:1

GGACACGGTG CGCTTGGCAA AGTGAACACC CAACAGAGAG GCGAAAGCGA GCCAAGACAC 60
 ACCACATACA CACGAAGAGA ACCAGCAAGA AGAAACCCGGT AGGCGGAGGA GGCGCTGCC 120
 CCAGTTCTC CAATATACCC AGCACCAT CACAAGCCCA GG ATG GAC AAC TGC 174
 Met Asp Asn Cys
 1
 GAC CAG GAC GCC AGC TTT CGG CTG AGC CAC ATC AAG GAG GAG GTC AAG 222
 Asp Gln Asp Ala Ser Phe Arg Leu Ser His Ile Lys Glu Glu Val Lys 20
 5 10 15 20
 CCG GAC ATC TCG CAG CTG AAC GAC AGC AAC AAC AGC AGC TTT TCG CCC 270
 Pro Asp Ile Ser Gln Leu Asn Asp Ser Asn Asn Ser Ser Phe Ser Pro 35
 25 30 35
 AAG GCC GAG AGT CCC GTG CCC TTC ATG CAG GCC ATG TCC ATG GTC CAC 318
 Lys Ala Glu Ser Pro Val Pro Phe Met Gln Ala Met Ser Met Val His 50
 40 45 50
 GTG CTG CCC GGC TCC AAC TCC GCC AGC TCC AAC AAC AAC AGC GCT GGA 366
 Val Leu Pro Gly Ser Asn Ser Ala Ser Ser Asn Asn Asn Ser Ala Gly 65
 55 60 65
 GAT GCC CAA ATG GCG CAG GCG CCC AAT TCG GCT GGA GGC TCT GCC GCC 414
 Asp Ala Gln Met Ala Gln Ala Pro Asn Ser Ala Gly Gly Ser Ala Ala 80
 70 75 80
 GCT GCA GTC CAG CAG CAG TAT CCG CCT AAC CAT CCG CTG AGC GGC AGC 462
 Ala Ala Val Gln Gln Gln Tyr Pro Pro Asn His Pro Leu Ser Gly Ser 100
 85 90 95 100
 AAG CAC CTC TGC TCT ATT TGC GGG GAT CGG GCC AGT GGC AAG CAC TAC 510
 Lys His Leu Cys Ser Ile Cys Gly Asp Arg Ala Ser Gly Lys His Tyr 115
 105 110 115
 GGC GTG TAC AGC TGT GAG GGC TGC AAG GGC TTC TTT AAA CGC ACA GTG 558
 Gly Val Tyr Ser Cys Glu Gly Cys Lys Gly Phe Phe Lys Arg Thr Val 130
 120 125 130
 CGC AAG GAT CTC ACA TAC GCT TGC AGG GAG AAC CGC AAC TGC ATC ATA 606
 Arg Lys Asp Leu Thr Tyr Ala Cys Arg Glu Asn Arg Asn Cys Ile Ile 145
 135 140 145
 GAC AAG CGG CAG AGG AAC CGC TGC CAG TAC TGC CGC TAC CAG AAG TGC 654
 Asp Lys Arg Gln Arg Asn Arg Cys Gln Tyr Cys Arg Tyr Gln Lys Cys 160
 150 155 160
 CTA ACC TGC GGC ATG AAG CGC GAA GCG GTC CAG GAG GAG CGT CAA CGC 702
 Leu Thr Cys Gly Met Lys Arg Glu Ala Val Gln Glu Glu Arg Gln Arg 180
 165 170 175 180
 GGC GCC CGC AAT GCG GCG GGT AGG CTC AGC GCC AGC GGA GGC GGC AGT 750
 Gly Ala Arg Asn Ala Ala Gly Arg Leu Ser Ala Ser Gly Gly Gly Ser 195
 185 190 195
 AGC GGT CCA GGT TCG GTA GGC GGA TCC AGC TCT CAA GGC GGA GGC GGA 798
 Ser Gly Pro Gly Ser Val Gly Gly Ser Ser Ser Gln Gly Gly Gly Gly 210
 200 205 210

45

GGA GGC GGC GTT TCT GGC GGA ATG GGC AGC GGC AAC GGT TCT GAT GAC Gly Gly Val Ser Gly Gly Met Gly Ser Gly Asn Gly Ser Asp Asp 215 220 225	846
TTC ATG ACC AAT AGC GTG TCC AGG GAT TTC TCG ATC GAG CCC ATC ATA Phe Met Thr Asn Ser Val Ser Arg Asp Phe Ser Ile Glu Arg Ile Ile 230 235 240	894
GAG GCC GAG CAG CGA GCG GAG ACC CAA TGC GGC GAT CGT GCA CTG ACG Glu Ala Glu Gln Arg Ala Glu Thr Gln Cys Gly Asp Arg Ala Leu Thr 245 250 255 260	942
TTC CTG CGC GTT GGT CCC TAT TCC ACA GTC CAG CCG GAC TAC AAG GGT Phe Leu Arg Val Gly Pro Tyr Ser Thr Val Gln Pro Asp Tyr Lys Gly 265 270 275	990
GCC GTG TCG GCC CTG TGC CAA GTG GTC AAC AAA CAG CTC TTC CAG ATG Ala Val Ser Ala Leu Cys Gln Val Val Asn Lys Gln Leu Phe Gln Met 280 285 290	1038
GTC GAA TAC GCG CGC ATG ATG CCG CAC TTT GCC CAG GTG CCG CTG GAC Val Glu Tyr Ala Arg Met Met Pro His Phe Ala Gln Val Pro Leu Asp 295 300 305	1086
GAC CAG GTG ATT CTG CTG AAA GCC GCT TGG ATC GAG CTG CTC ATT GCG Asp Gln Val Ile Leu Leu Lys Ala Ala Trp Ile Glu Leu Leu Ile Ala 310 315 320	1134
AAC GTG GCC TGG TGC AGC ATC GTT TCG CTG GAT GAC GGC GGT GCC GGC Asn Val Ala Trp Cys Ser Ile Val Ser Leu Asp Asp Gly Gly Ala Gly 325 330 335 340	1182
GGC GGG GGC GGT GGA CTA GGC CAC GAT GGC TCC TTT GAG CGA CGA TCA Gly Gly Gly Gly Leu Gly His Asp Gly Ser Phe Glu Arg Arg Ser 345 350 355	1230
CCG GGC CTT CAG CCC CAG CTG TTC CTC AAC CAG AGC TTC TCG TAC Pro Gly Leu Gln Pro Gln Leu Phe Leu Asn Gln Ser Phe Ser Tyr 360 365 370	1278
CAT CGC AAC AGT GCG ATC AAA GCC GGT GTG TCA GCC ATC TTC GAC CGC His Arg Asn Ser Ala Ile Lys Ala Gly Val Ser Ala Ile Phe Asp Arg 375 380 385	1326
ATA TTG TCG GAG CTG AGT GTA AAG ATG AAG CGG CTG AAT CTC GAC CGA Ile Leu Ser Glu Leu Ser Val Lys Met Lys Arg Leu Asn Leu Asp Arg 390 395 400	1374
CGC GAG CTG TCC TGC TTG AAG GCC ATC ATA CTG TAC AAC CCG GAC ATA Arg Glu Leu Ser Cys Leu Lys Ala Ile Ile Leu Tyr Asn Pro Asp Ile 405 410 415 420	1422
CGC GGG ATC AAG AGC CGG GCG GAG ATC GAG ATG TGC CGC GAG AAG GTG Arg Gly Ile Lys Ser Arg Ala Glu Ile Glu Met Cys Arg Glu Lys Val 425 430 435	1470
TAC GCT TGC CTG GAC GAG CAC TGC CGC CTG GAA CAT CCG GGC GAC GAT Tyr Ala Cys Leu Asp Glu His Cys Arg Leu Glu His Pro Gly Asp Asp 440 445 450	1518
GGA CGC TTT GCG CAA CTG CTG CGT CTG CGC CGC TTT GCG ATC GAT Gly Arg Phe Ala Gln Leu Leu Arg Leu Arg Arg Phe Ala Ile Asp 455 460 465	1566
CAG CCT GAA GTG CCA GGA TCA CCT GTT CCT CTT CCG CAT TAC CAG CGA Gln Pro Glu Val Pro Gly Ser Pro Val Pro Leu Pro His Tyr Gln Arg 470 475 480	1614

CCG GCC GCT GGA GGA GCT CTT TCT CGA GCA GCT GGA GGC GCC GCC GCC Pro Ala Ala Gly Gly Ala Leu Ser Arg Ala Ala Gly Gly Ala Ala Ala 485 490 495 500	1662
ACC CGG CCT GGC GAT GAA ACT GGA GTA GGG TCC CGA CTC T AAAGTCGGCC Thr Arg Pro Gly Asp Glu Thr Gly Val Gly Ser Arg Leu 505 510	1712
CCGTTCTCCA TCCGAAAAAT GTTTCATTGT GATTGGCTTT GTTTGCATTCTCCTCTCTA TCCCTACAAA AGCCCCCTAA TATTACGCAA AATGTGTATG TAATTGTTA TTTTTTTTT ATTACCTAAT ATTATTATTA TTATTGATAT AGAAAATGTT TTCCCTTAAGA TGAAGATTAG CCTCCTCGAC GTTTATGTCC CAGTAAACGA AAAACAAACA AAATCCAAAAA CTTGAAAAGA ACACAAAACA CGAACGAGAA AATGCCACACA AGCAAAGTAA AAGTAAAAGT TAAACTAAAG CTAAACGAGT AAAGATATTA AAATAACGGT TAAAATTAAT GCATAGTTAT GATCTACAGA CGTATGTAAA CATACTAAATT CAGCATAAAAT ATATATGTCA GCAGGCGCAT ATCTGCCGTG CTGGCCCCGT TCTAAACCAA TTGTAATTAC TTTTTAACAT AAATTTACCC AAAACGTTAT CAATTAGATG CGAGATACAA AAATCACCGA CGAAAACCAA CAAAATATAT CTATGTATAA AAAATATAAG CTGCATAACA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AA	1772 1832 1892 1952 2012 2072 2132 2192 2252 2304

SEQ ID NO:2 [TO BE GENERATED BY PATENTIN FROM SEQ ID NO:1]

SEQ ID NO:3

Cys - X - X - Cys - X - X - Asp* - X - Ala* - X - Gly*
 - X - Tyr* - X - X - X - X - Cys - X - X - Cys - Lys* -
 X - Phe - Phe - X - Arg* - X - X - X - X - X - X - X -
 X - X - (X - X -) Cys - X - X - X - X - X - (X - X - X
 -) Cys - X - X - X - Lys - X - X - Arg - X - X - Cys - X
 - X - Cys - Arg* - X - X - Lys* - Cys - X - X - X -
 Gly* - Met,

SEQ ID No:4 5'-AGGTCA-AGG-AGGTCA-3',

SEQ ID No:5 5'-GGGTGA-ATG-AGGACA-3',

SEQ ID No:6 5'-GGGTGA-ACG-GGGGCA-3',

SEQ ID No:7 5'-GGTTCA-CGA-GGTTCA-3',

SEQ ID No:8 5'-AGGTCA-CAGG-AGGTCA-3',

SEQ ID No:9 5'-AGGTGA-CAGG-AGGTCA-3',

SEQ ID No:10 5'-AGGTGA-CAGG-AGGACA-3',

SEQ ID No:11 5'-GGGTTA-GGGG-AGGACA-3',

SEQ ID No:12 5'-GGGTCA-TTTC-AGGTCC-3',

SEQ ID No:13 5'-AGGTCA-CCAGG-AGGTCA-3',

SEQ ID No:14 5'-AGGTGA-ACAGG-AGGTCA-3',

SEQ ID No:15 5'-GGTTCA-CCGAA-AGTTCA-3',

SEQ ID No:16 5'-GGTTCA-CCGAA-AGTTCA-3',

SEQ ID No:17 5'-AGGTCA-CTGAC-AGGGCA-3',
SEQ ID No:18 5'-GGGTCA-TTCAG-AGTTCA-3',
SEQ ID No:19 5'-AAGCTTAAG-GGTTCA-CCGAA-AGTTCA-CTCAGCTT-3',
SEQ ID No:20 5'-AAGCTTAAG-GGTTCA-CCGAA-AGTTCA-CTCGCATAGCTT-3',
SEQ ID No:21 5'-AAGCTTAAG-GGTTCA-CCGAA-AGTTCA-
CTCGCATATATTACCTT-3'.
SEQ ID NO:22 5'-AGCTCGATGG ACAAGTGCAT TGAACCCTTG AGCTACCTGT TCACGTAACT
TGGGAACCTTC GA,
SEQ ID NO:23 5'-CCTGGGCCAC GGCGGCCGCC GGAGCTGTG CCTG,
SEQ ID NO:24 5'-GTGGGTATG CGCCTCGAGT GCGTCGTCCC,
SEQ ID NO:25 5'-AGGACAAAGG TCA,
SEQ ID NO:26 ATTGGACAAGTGCATTGAACCCCTTGTCTCT
TAACCAGTTACGTAACCTGGGAACAGAGA
SEQ ID NO:27 atgctGTGCATTGAACGtgctcga
tacgaCACGTAACCTTGcacgagct
SEQ ID NO:28 atgAAGTGCATTGAACCCgctcga
tacTTCACGTAACCTGGGcgagct
SEQ ID NO:29 TAAAGGATCTTGACCCCAATGAACCTCTTA
ATTCCTAGAACTGGGTTACTTGAAGAAT